SEQUENCE LISTING

GENERAL INFORMATION

<110> APPLICANT: The Regents of the University of California
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Campos, Reinaldo
Nonogaki, Hiroyuki
Suslow, Trevor

<120> TITLE OF INVENTION: Characteristics of Phenylalanine Ammonia-lyase (PAL) Gene in Wounded Lettuce Tissue

<130> FILE REFERENCE: UCDA.004.01US

<140> CURRENT APPLICATION NUMBER: 09/964,992

<141> CURRENT FILING DATE: 2001-09-26

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<160> NUMBER OF SEQ ID NOS: 5

<170> SOFTWARE: PatentIn version 3.0

<210> SEQ ID NO: 1

<211> LENGTH: 711

<212> TYPE: PRT

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE: 1

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Met Glu Asn Gly Asn His Val Asn Gly Val Val Asn Glu Leu Cys Ile
1               5                  10                  15

Lys Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Leu Thr Gly Ser
            20                  25                  30

His Leu Asp Glu Val Lys Lys Met Val Ala Glu Phe Arg Lys Pro Val
        35                  40                  45

Val Lys Leu Gly Gly Glu Thr Leu Thr Val Ser Gln Val Ala Gly Ile
    50                  55                  60

Ala Ala Ala Asn Asp Ser Asp Thr Val Lys Val Glu Leu Ser Glu Ala
65                  70                  75                  80

Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met
                85                  90                  95

Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr
            100                 105                 110

Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile
        115                 120                 125

Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Thr Ser His
    130                 135                 140

Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Ile Val Arg Ile Asn
145                 150                 155                 160

Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Gln Ile Leu Glu Ala
                165                 170                 175

Ile Thr Lys Phe Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu Arg
            180                 185                 190

Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
        195                 200                 205

Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Thr Gly
    210                 215                 220

Glu Val Leu Asn Ala Glu Lys Ala Phe Ala Ala Ala Gly Val Glu Gly
225                 230                 235                 240

Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly
                245                 250                 255

Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu Phe Asp Ala Asn
            260                 265                 270

Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val
        275                 280                 285
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Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys
290 295 300

His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu Tyr Ile Leu
305 310 315 320

Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val His Glu Met Asp
325 330 335

Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
340 345 350

Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser Ser Thr Lys Met
355 360 365

Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
370 375 380

Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile
385 390 395 400

Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
405 410 415

Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn
420 425 430

Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Tyr
435 440 445

Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
450 455 460

Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
465 470 475 480

His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
485 490 495

Ala Glu Ala Val Asp Ile Leu Lys Leu Met Ser Ser Thr Tyr Leu Val
500 505 510

Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu Glu Glu Asn Met Lys
515 520 525

Ser Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Lys Val Leu Thr
530 535 540

Met Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp
545 550 555 560

Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ile Asp Asp
565 570 575

Val Cys Ser Gly Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu
580 585 590

Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Thr Asn Thr

595 600 605

Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Glu Glu Leu Lys Val Leu
610 615 620

Leu Pro Lys Glu Val Glu Gly Val Arg Ile Ala Tyr Glu Asn Asp Thr
625 630 635 640

Leu Ser Ile Pro Asn Arg Ile Lys Ala Cys Arg Ser Tyr Pro Leu Tyr
645 650 655

Arg Phe Val Arg Glu Glu Leu Gly Arg Gly Phe Leu Thr Gly Glu Lys
660 665 670

Val Thr Ser Pro Gly Glu Glu Phe Asp Arg Val Phe Thr Ala Met Cys
675 680 685

Lys Gly Gln Ile Ile Asp Pro Leu Leu Glu Cys Leu Gly Gly Trp Asn
690 695 700

Gly Glu Pro Leu Pro Ile Cys
705 710

<210> SEQUENCE ID NO: 2

<211> LENGTH: 712

<212> TYPE: PRT

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE 2

Met Gly Ser Thr Glu Met Glu Val Asp Ser His Gln Asn Gly Glu Arg
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Ala Glu Phe Cys Val Gly Asp Pro Leu Asn Trp Gly Met Ala Ala Glu
20 25 30

Ser Leu Lys Gly Ser His Leu Asp Glu Val Lys Arg Met Val Ala Glu
35 40 45

Phe Arg Lys Pro Val Val Arg Leu Gly Gly Glu Thr Leu Thr Val Ser
50 55 60

Gln Val Ala Ala Ile Ala Ala Ser Asp Asn Ala Gly Val Lys Val Glu
65 70 75 80

Leu Ser Glu Thr Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val
85 90 95

Met Glu Ser Met Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly
100 105 110

Phe Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln
115 120 125

Lys Glu Leu Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr

```
     130                 135                 140

Glu Ser Thr His Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Leu
145                 150                 155                 160

Val Arg Ile Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu
                165                 170                 175

Ile Leu Glu Ala Ile Thr Lys Phe Leu Asn His Asn Val Thr Pro Phe
            180                 185                 190

Leu Pro Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu
        195                 200                 205

Ser Tyr Ile Ala Gly Leu Leu Thr Gly Arg Ala Asn Ser Lys Ala Val
    210                 215                 220

Gly Pro Thr Gly Glu Val Leu Asn Ala Glu Lys Ala Phe Ala Glu Ala
225                 230                 235                 240

Gly Val Glu Gly Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala
                245                 250                 255

Leu Val Asn Gly Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu
            260                 265                 270

Phe Asp Ala Asn Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile
        275                 280                 285

Phe Ala Glu Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr
    290                 295                 300

His Lys Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met
305                 310                 315                 320

Glu Tyr Ile Leu Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val
                325                 330                 335

His Glu Met Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu
            340                 345                 350

Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser
        355                 360                 365

Ser Thr Lys Met Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro
    370                 375                 380

Leu Ile Asp Val Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln
385                 390                 395                 400

Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala
                405                 410                 415

Ala Ile Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp
            420                 425                 430

Thr Tyr Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro
        435                 440                 445
```

Ser Leu Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr
450 455 460

Cys Ser Glu Leu Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln
465 470 475 480

Ser Ala Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser
485 490 495

Ala Arg Lys Thr Ala Glu Ser Val Glu Ile Leu Lys Leu Met Ser Thr
500 505 510

Thr Tyr Leu Val Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu Glu
515 520 525

Glu Asn Leu Lys Ser Thr Val Lys Asn Thr Val Ser Leu Val Ala Lys
530 535 540

Lys Ile Leu Thr Thr Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe
545 550 555 560

Cys Glu Lys Asp Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala
565 570 575

Tyr Ile Asp Asp Ala Cys Ser Ala Thr Tyr Pro Leu Met Gln Lys Leu
580 585 590

Arg Gln Val Ile Val Asp His Ala Leu Asn Asn Glu Asn Asp Ala Gly
595 600 605

Thr Ser Ile Phe Gln Lys Ile Ser Glu Phe Glu Glu Glu Leu Lys Ala
610 615 620

Val Leu Pro Lys Glu Val Glu Gly Val Arg Ser Ala Tyr Glu Ser Ser
625 630 635 640

Thr Leu Thr Ile Pro Asn Arg Ile Lys Glu Cys Arg Ser Tyr Pro Leu
645 650 655

Tyr Arg Phe Val Arg Glu Glu Leu Gly Thr Gly Phe Leu Thr Gly Glu
660 665 670

Glu Val Thr Ser Pro Gly Glu Glu Phe Asp Lys Val Phe Thr Ala Leu
675 680 685

Lys Lys Gly His Ile Ile Asp Pro Leu Leu Glu Cys Val Gln Gly Trp
690 695 700

Asn Gly Val Pro Leu Pro Ile Ser
705 710

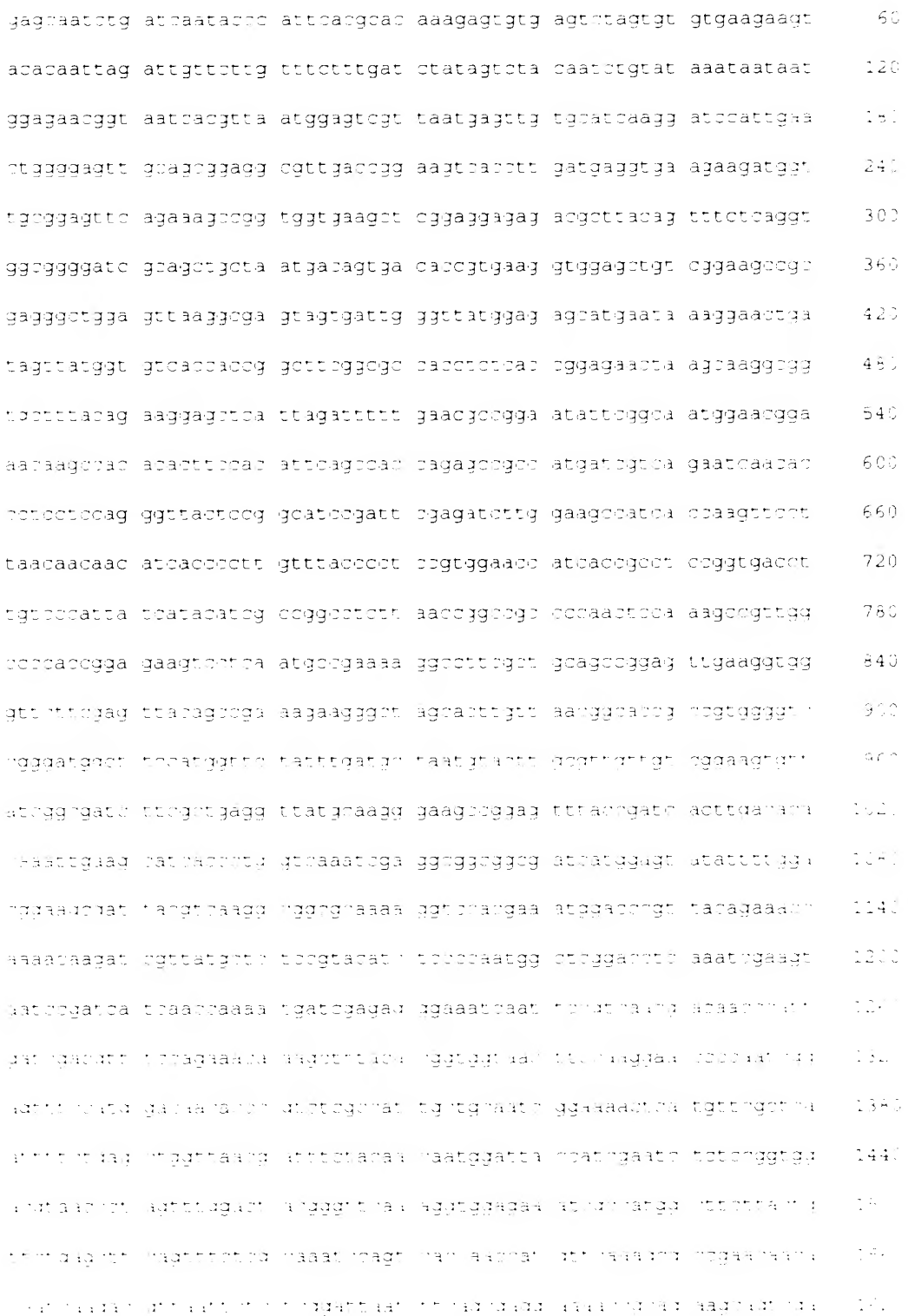
(210) SEQ ID NO: 3

(211) LENGTH: 2442

(212) TYPE: cDNA

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE 3



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ccatttggaa gagaacatga aatcgacagt gaagaacacc gtaagccaag tcgcgaaaaa 1740

ggtcctcacc atgggcgtca acggcgagct ccacccgtcg agattctgcg agaaagatct 1800

cctccgtgtt gttgatcgtg aatacgtctt cgcttacatc gacgacgttt gcagcggcac 1860

atacccatta atgcagaagc tccgacaggt tctggtcgac cacgctctaa acaacggcga 1920

aacggagaag aacactaaca cctccatctt ccaaaagatc gctacctttg aagaagaatt 1980

gaaagtcctg ttaccgaaag aagttgaagg tgttagaatc gcttatgaga atgatacatt 2040

gtcgattcca aacaggatta aagcttgcag atcgtacccg ttgtataggt ttgtaaggga 2100

ggagctcggc agagggtttt tgaccggaga aaaggtgacg tcgccgggag aggagttcga 2160

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agggtggaat ggggaacctc ttccaatatg ttaggaaagt gagtgtgaaa ccgtttgaat 2280

tgtatttgta atattctgtt tttttttttt tttttaaat tttatttgca tttaatatct 2340

catcaaagac ttccactttc aagtgtggtg tatgtggttg taaatcatat atattaactt 2400

attattttg ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2442

<210> SEQ ID NO: 4

<211> LENGTH: 2380

<212> TYPE: cDNA

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE 4

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aaaggctagt catttagacg aggtgaagcg gatggtggcg gagtttagga agccggtggt 240

gagattgggt ggagagacgt tgactgtgtc gcaggtggcg gcgatcgctg ccagtgataa 300

cgctggggtg aaggtggaac tgtcggagac ggcgagggcg ggggtgaagg cgagtagtga 360

[illegible] gagagtatga ataaaggaac ggatagctat ggtgtcacta ccgggttcgg 420

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cacaagagca gccatgcttg tcagaatcaa cacccttctt caaggttact ccggcatccg 600

attcgagatc ttggaggcga tcaccaagtt cctcaaccac aacgtcaccc cttttctccc 660

tctccgtggg acaattaccg cctccggcga tctcgtccca ttatcctaca tcgccggtct 720

tctcaccggc cgtgccaact ccaaagccgt tggacccacc ggagaagttc taaatgccga 780

aaaggccttc gcggaagccg gagttgaagg tggtttcttc gagttacagc cgaaagaagg 840

gctagcactt gtcaacggca ccgccgtggg atccgggatg gcgtcgatgg tgctatttga 900

tgctaatgtt cttgcattgt tgtcggaagt gttatcggcg atcttcgctg aagttatgca 960

aggtaagccg gagtttactg atcacttaac acacaaattg aagcatcacc ccggtcaaat 1020

cgaggcggcg gcgatcatgg agtatatttt ggacggaagc gattacgtca aggcggcgca 1080

aaaggtccac gaaatggacc cgttacagaa accaaaacaa gatcgttatg ctctccgtac 1140

atctccccaa tggctcggac ctcaaatcga agtaatccga tcatcaacca aaatgatcga 1200

gagagaaatc aactccgtca acgacaaccc attgatcgac gtttccagaa acaaagcctt 1260

acacggtggc aacttccaag gaaccccaat cggagtttcc atggataaca cacgtttggc 1320

gatcgccgcc atcggaaagc taatgttcgc tcagttctct gagcttgtca acgattttta 1380

caacaacggg ttgccatcca atctctccgg cggccggaat ccaagtttgg attacgggtt 1440

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gatttcagca agaaaaacag cagaatcagt cgagatctta aaactcatgt caaccacatа 1620

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ctttgcatac atcgacgacg cttgcagcgc cacctaccca ttgatgcaga agctccgaca 1860

ggttatcgtc gaccacgcat taaacaatga aaatgagcct ggaacttcca tctttcaaaa 1920

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aagtacatac gagagtttga cattgacgat tccaaacagg atcaaggagt gtagatcata 2040

ccattgtac aggtttgtga gagaggagct tggaacaggg tttttgacag gggaggaggt 2100

gacgtcacct ggagaagagt tcgataaggt gttcactgct ttgtgcaaag gacatattat 2160

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caaatgtgta tgtaattgta atgtactatt gtatgtttgt aattgtacca cgttaagtgt 2340

acctttgtt tcataaaaaa aaaaaaaaaa aaaaaaaaaa 2380

<210> SEQ ID NO: 5

<211> LENGTH: 666

<212> TYPE: PRT

<213> ORGANISM: Common Sunflower (Helianthus annuus)

<400> SEQUENCE 5

Met Glu Asn Gly Thr His Val Asn Gly Ser Ala Asn Gly Phe Cys Ile
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Lys Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Leu Thr Gly Ser
20 25 30

His Leu Asp Glu Val Lys Lys Met Val Gly Glu Phe Arg Lys Pro Val
35 40 45

Val Lys Leu Gly Gly Glu Thr Leu Thr Val Ser Gln Val Ala Gly Ile
50 55 60

Ser Ala Ala Gly Asp Gly Asn Met Val Lys Val Glu Leu Ser Glu Ala
65 70 75 80

Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met
85 90 95

Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr
100 105 110

Ser His Arg Arg Thr Lys Asn Gly Gly Ala Leu Gln Lys Glu Leu Ile
115 120 125

Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Ser His
130 135 140

Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Ile Val Arg Ile Asn
145 150 155 160

Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala
165 170 175

Ile Thr Lys Phe Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu Arg
180 185 190

Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
195 200 205

Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Ala Gly
210 215 220

Glu Val Leu Asn Ala Glu Ser Ala Thr Ala Gln Ala Gly Val Glu Gly

225 230 235 240

Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly
245 250 255

Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu Phe Glu Ala Asn
260 265 270

Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val
275 280 285

Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys
290 295 300

His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu Tyr Ile Leu
305 310 315 320

Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val His Glu Met Asp
325 330 335

Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
340 345 350

Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser Ala Thr Lys Met
355 360 365

Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
370 375 380

Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile
385 390 395 400

Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
405 410 415

Val Thr Ile Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn
420 425 430

Gly Leu Pro Ser His Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Ser
435 440 445

Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
450 455 460

Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
465 470 475 480

His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
485 490 495

Ala Glu Ala Val Asp Ile Leu Lys Leu Met Ser Ser Thr Tyr Leu Val
500 505 510

Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu Glu Glu Asn Met Lys
515 520 525

Thr Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Lys Val Leu Thr
530 535 540

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Met Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp
545                 550                 555                 560

Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ala Asp Asp
                565                 570                 575

Pro Cys Leu Thr Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu
            580                 585                 590

Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Ala Asn Thr
        595                 600                 605

Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala Ile
    610                 615                 620

Leu Pro Lys Glu Val Glu Ser Val Arg Val Ala Phe Glu Asn Gly Thr
625                 630                 635                 640

Met Ser Ile Pro Asn Arg Ile Lys Ala Cys Arg Ser Tyr Pro Leu Tyr
                645                 650                 655

Arg Phe Val Arg Glu Glu Leu Gly Gly Ala
            660                 665
```